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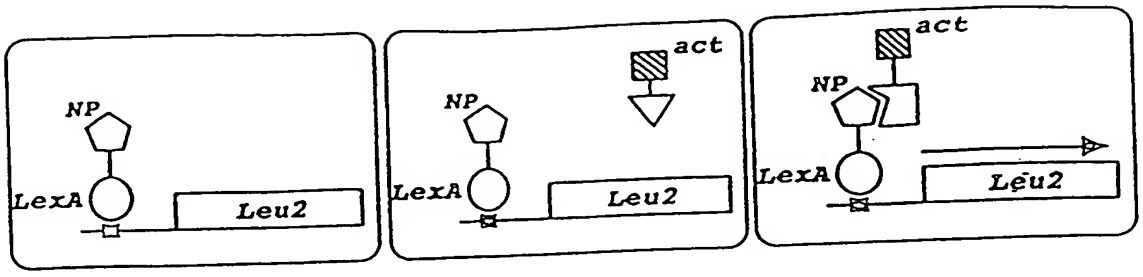
NP
LexA
Leu2
act
NP
LexA
Leu2
act
NP
LexA
Leu2

FIG. 1A

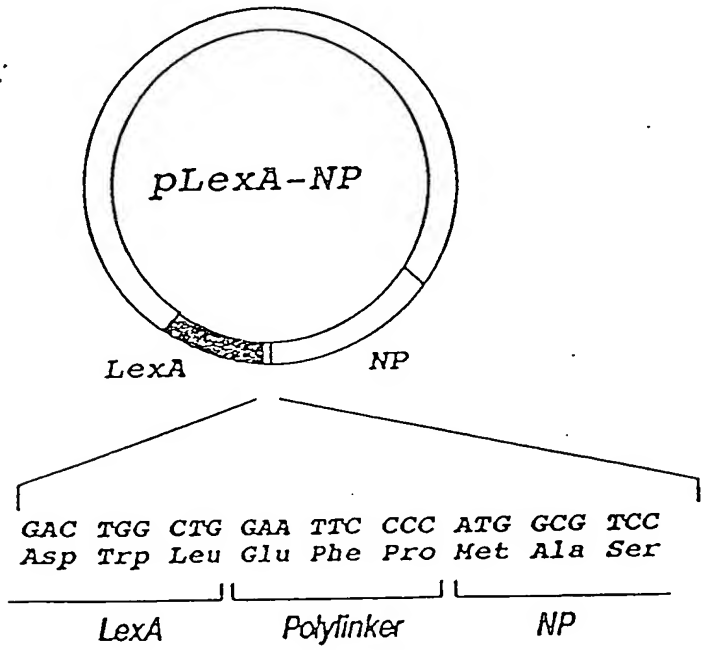
pLexA-NP
LexA
NP
GAC TGG CTG GAA TTC CCC ATG GCG TCC
Asp Trp Leu Glu Phe Pro Met Ala Ser
LexA
Polylinker
NP

FIG. 1B

```
                    20                  40                  60
CTAACTTCAG CGGTGGCACC GGGATCGGTT GCCTTGAGCC TGAAATATGA CCACCCCAGG
                                                  M   T  T  P  G>

                    80                 100                 120
AAAAGAGAAC TTTCGCCTGA AAAGTTACAA GAACAAATCT CTGAATCCCG ATGAGATGCG
  K  E  N   F  R  L   K  S  Y  K   N  K  S   L  N  P   D  E  M  R>

                   140                 160                 180
CAGGAGGAGG GAGGAAGAAG GACTGCAGTT ACGAAAGCAG AAAAGAGAAG AGCAGTTATT
  R  R  R   E  E  E   G  L  Q  L   R  K  Q   K  R  E   E  Q  L  F>

                   200                 220                 240
CAAGCGGAGA AATGTTGCTA CAGCAGAAGA AGAAACAGAA GAAGAAGTTA TGTCAGATGG
  K  R  R   N  V  A   T  A  E  E   E  T  E   E  E  V   M  S  D  G>

                   260                 280                 300
AGGCTTTCAT GAGGCTCAGA TTAGTAACAT GGAGATGGCA CCAGGTGGTG TCATCACTTC
  G  F  H   E  A  Q   I  S  N  M   E  M  A   P  G  G   V  I  T  S>

                   320                 340                 360
TGACATGATT GAGATGATAT TTTCCAAAAG CCCAGAGCAA CAGCTTTCAG CAACACAGAA
  D  M  I   E  M  I   F  S  K  S   P  E  Q   Q  L  S   A  T  Q  K>

                   380                 400                 420
ATTCAGGAAG CTGCTTTCAA AAGAACCTAA CCCTCCTATT GATGAAGTTA TCAGCACACC
  F  R  K   L  L  S   K  E  P  N   P  P  I   D  E  V   I  S  T  P>

                   440                 460                 480
AGGAGTAGTG GCCAGGTTTG TGGAGTTCCT CAAACGAAAA GAGAATTGTT CACTGCAGTT
  G  V  V   A  R  F   V  E  F  L   K  R  K   E  N  C   S  L  Q  F>

                   500                 520                 540
TGAATCAGCT TGGGTACTGA CAAATATTGC TTCAGGAAAT TCTCTTCAGA CCCGAATTGT
  E  S  A   W  V  L   T  N  I  A   S  G  N   S  L  Q   T  R  I  V>

                   560                 580                 600
GATTCAGGCA AGAGCTGTGC CCATCTTCAT AGAGTTGCTC AGCTCAGAGT TTGAAGATGT
  I  Q  A   R  A  V   P  I  F  I   E  L  L   S  S  E   F  E  D  V>

                   620                 640                 660
CCAGGAACAG GCAGTCTGGG CTCTTGGCAA CATTGCTGGA GATAGTACCA TGTGCAGGGA
  Q  E  Q   A  V  W   A  L  G  N   I  A  G   D  S  T   M  C  R  D>

                   680                 700                 720
CTATGTCTTA GACTGCAATA TCCTTCCCCC TCTTTTGCAG TTATTTTCAA AGCAAAACCG
  Y  V  L   D  C  N   I  L  P  P   L  L  Q   L  F  S   K  Q  N  R>

                   740                 760                 780
CCTGACCATG ACCCGGAATG CAGTATGGGC TTTGTCTAAT CTCTGTAGAG GGAAAAGTCC
  L  T  M   T  R  N   A  V  W  A   L  S  N   L  C  R   G  K  S  P>
```

FIG. 2A

```
                    800                 820                 840
ACCTCCAGAA TTTGCAAAGG TTTCTCCATG TCTGAATGTG CTTTCCTGGT TGCTGTTTGT
  P  P  E  F  A  K  V  S  P  C  L  N  V  L  S  W  L  L  F  V>

                    860                 880                 900
CAGTGACACT GATGTACTGG CTGATGCCTG CTGGGCCCTC TCATATCTAT CAGATGGACC
  S  D  T  D  V  L  A  D  A  C  W  A  L  S  Y  L  S  D  G  P>

                    920                 940                 960
CAATGATAAA ATTCAAGCGG TCATCGATGC GGGAGTATGT AGGAGACTTG TGGAACTGCT
  N  D  K  I  Q  A  V  I  D  A  G  V  C  R  R  L  V  E  L  L>

                    980                1000                1020
GATGCATAAT GATTATAAAG TGGTTTCTCC TGCTTTGCGA GCTGTGGGAA ACATTGTCAC
  M  H  N  D  Y  K  V  V  S  P  A  L  R  A  V  G  N  I  V  T>

                   1040                1060                1080
AGGGGATGAT ATTCAGACAC AGGTAATTCT GAATTGCTCA GCTCTGCAGA GTTTATTGCA
  G  D  D  I  Q  T  Q  V  I  L  N  C  S  A  L  Q  S  L  L  H>

                   1100                1120                1140
TTTGCTGAGT AGCCCAAAGG AATCTATCAA AAAGGAAGCA TGTTGGACGA TATCTAATAT
  L  L  S  S  P  K  E  S  I  K  K  E  A  C  W  T  I  S  N  I>

                   1160                1180                1200
TACAGCTGGA AATAGGGCAC AGATCCAGAC TGTGATAGAT GCCAACATTT TCCCAGCCCT
  T  A  G  N  R  A  Q  I  Q  T  V  I  D  A  N  I  F  P  A  L>

                   1220                1240                1260
CATTAGTATT TTACAAACTG CTGAATTTCG GACAAGAAAA GAAGCAGCTT GGGCCATCAC
  I  S  I  L  Q  T  A  E  F  R  T  R  K  E  A  A  W  A  I  T>

                   1280                1300                1320
AAATGCAACT TCTGGAGGAT CAGCTGAACA GATCAAGTAC CTAGTAGAAC TGGGTTGTAT
  N  A  T  S  G  G  S  A  E  Q  I  K  Y  L  V  E  L  G  C  I>

                   1340                1360                1380
CAAGCCGCTC TGTGATCTCC TCACGGTCAT GGACTCTAAG ATTGTACAGG TTGCCCTAAA
  K  P  L  C  D  L  L  T  V  M  D  S  K  I  V  Q  V  A  L  N>

                   1400                1420                1440
TGGCTTGGAA AATATCCTGA GGCTTGGAGA ACAGGAAGCC AAAAGGAACG GCACTGGCAT
  G  L  E  N  I  L  R  L  G  E  Q  E  A  K  R  N  G  T  G  I>

                   1460                1480                1500
TAACCCTTAC TGTGCTTTGA TTGAAGAAGC TTATGGTCTG GATAAAATTG AGTTCTTACA
  N  P  Y  C  A  L  I  E  E  A  Y  G  L  D  K  I  E  F  L  Q>

                   1520                1540                1560
GAGTCATGAA AACCAGGAGA TCTACCAAAA GGCCTTTGAT CTTATTGAGC ATTACTTCGG
  S  H  E  N  Q  E  I  Y  Q  K  A  F  D  L  I  E  H  Y  F  G>

                   1580                1600                1620
GACCGAAGAT GAAGACAGCA GCATTGCACC CCAGGTTGAC CTTAACCAGC AGCAGTACAT
  T  E  D  E  D  S  S  I  A  P  Q  V  D  L  N  Q  Q  Q  Y  I>
```

FIG. 2B

```
                                  1640                   1660                   1680
CTTCCAACAG TGTGAGGCTC CTATGGAAGG TTTCCAGCTT TGAAGCAATA CTCTGCTTTC
 F - Q  Q   C  E  A   P  M  E  G   F  Q  L>
                                  1700                   1720                   1740
ACGTACCTGT GCTCAGACCA GGCTACCCAG TCGAGTCCTC TTGTGGAGCC CACAGTCCTC
                                  1760                   1780                   1800
ATGGAGCTAA CTTCTCAAAT GTTTTCCATA ATACTGTTTG CGCTCATTTG CTTGCCTTGC
                                  1820                   1840                   1860
GCACCTGCTC TCTTACACAC ATCTGGAAAA CCTCCGGCTC TCTGTGGTGG GATACCCTTC
                                  1880                   1900                   1920
TAATAAAAGG GTAACCAGAA CGGCCCACTC TCTTTTACGG AAAAATCCCT AGGCTTTGGA
                                  1940                   1960                   1980
GATCCGCACT TACATTAGAG TTATGGGAAT ATACACATAT TAATGTGGCT CCCTTTTTCT
                                  2000                   2020                   2040
TGTGGGGGAA TAAAAGAGGA CTCCTCCTCA TTCCCTTTAA CATGGGGGAA AAAACTGACA
                                  2060                   2080                   2100
TTAAAAGATG AGACTAAATC TTTATCTTGA ATTTTACACA ACTACTTACG ACAAGGGAGA
                                  2120                   2140                   2160
TGTTTAGACC TGTTGGTATA CTTCAGAGTA CTTTTCATGA GTTCTTCCAC AGTGAACCCT
                                  2180                   2200                   2220
TGGATTACCT GGTGGCTTTT TCTAGCCAGA TTGCATTAAT CCTTACTGAG ATTGGATGGT
                                  2240                   2260                   2280
TTTCTTTCCT CTATTGGCGC CATTCTTCAG ATATTAAAGT TAAACCATCC ACTCCCTCAC
                                  2300                   2320                   2340
CTTCAGCCTT CAGTGAATGT GCTTTCTAGT TGTCAGGAAT GCTGAAGAAT TAACACTTTG
                                  2360                   2380                   2400
ACTCCTAAAT GTGATACTGG TGGGTAAGAG CAGGGCACAT TTAATTTGTT CGCTTTTGCT
                                  2420                   2440                   2460
TCTCTTTGGT CTGGGCACAT TTAATTTGTT CGCTTTTGCT TCTCTTTGGT CTTTTCGAAT
                                  2480                   2500                   2520
ACTTAGTAAT CGAAAACCAT ATCCTGTAAT TTAATAAAAA AAACTAAGGA CGAAAAAACC
                                  2540                   2560                   2580
CCTCCAATTT TCCCAAATGC AATCAGTGTA ACTAGGGGCT GTGTTTCTGC ATTAAAATAA
                                  2600                   2620                   2640
ATGTTTCAGG CTTTGTGGTC CTGATCAAGG TCCTCATTAA AAAATTGGAG TTCACCCTAG
                                  2660                   2680                   2700
GCTTTTCCCC TCTGTGACTG GCAGATAACA CATACTTTTG AAAGTAACTT TGGGATTTTT
```

FIG. 2C

```
                    2720                    2740                    2760
TTTCTTAGGT GCAGCTCGAT TCTAATCTTT TCATGCTGCA CACGATTCCT TTAATCGATA

                    2780                    2800                    2820
GCATCCTTAT CTGAAAGAAA TAACCATCTT CTCAACATGA CCTGCTTAAC CCAAATAAGA

                    2840                    2860                    2880
ACAGTGATCT TATAACCTCA TTGTTTCCTA ATCTATTTTA TTTCATCTCC TGCTAGTACT

                    2900                    2920                    2940
GTGCCGCTTC CCCCTCCCCC CACACAAAAT AAAAACAGTA TCTCGCTTCT GGCTCATTTT
```

FIG. 2D

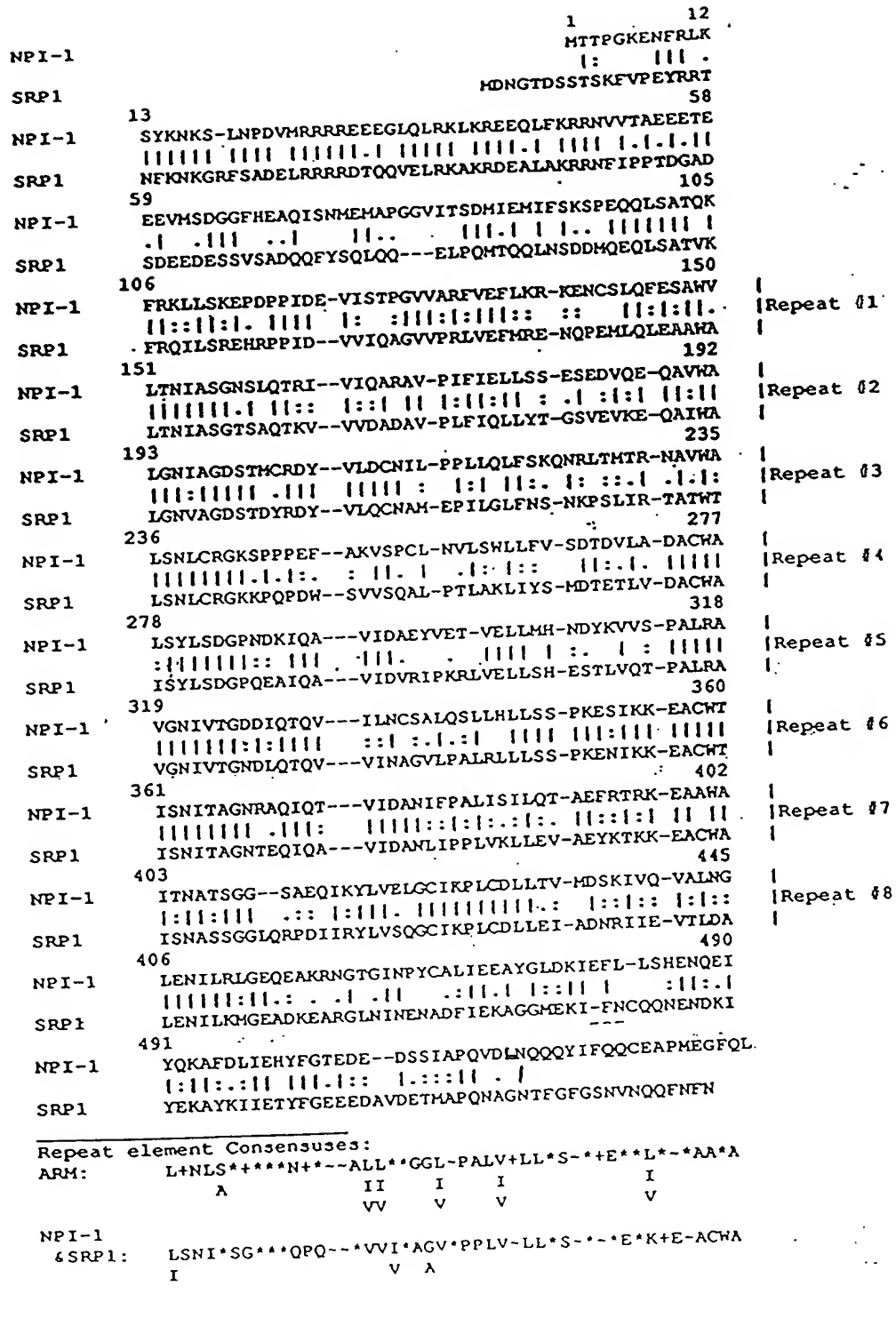
NPI-1
SRP1
Repeat #1
Repeat #2
Repeat #3
Repeat #4
Repeat #5
Repeat #6
Repeat #7
Repeat #8
Repeat element Consensuses:
ARM:
NPI-1
&SRP1:

FIG. 3

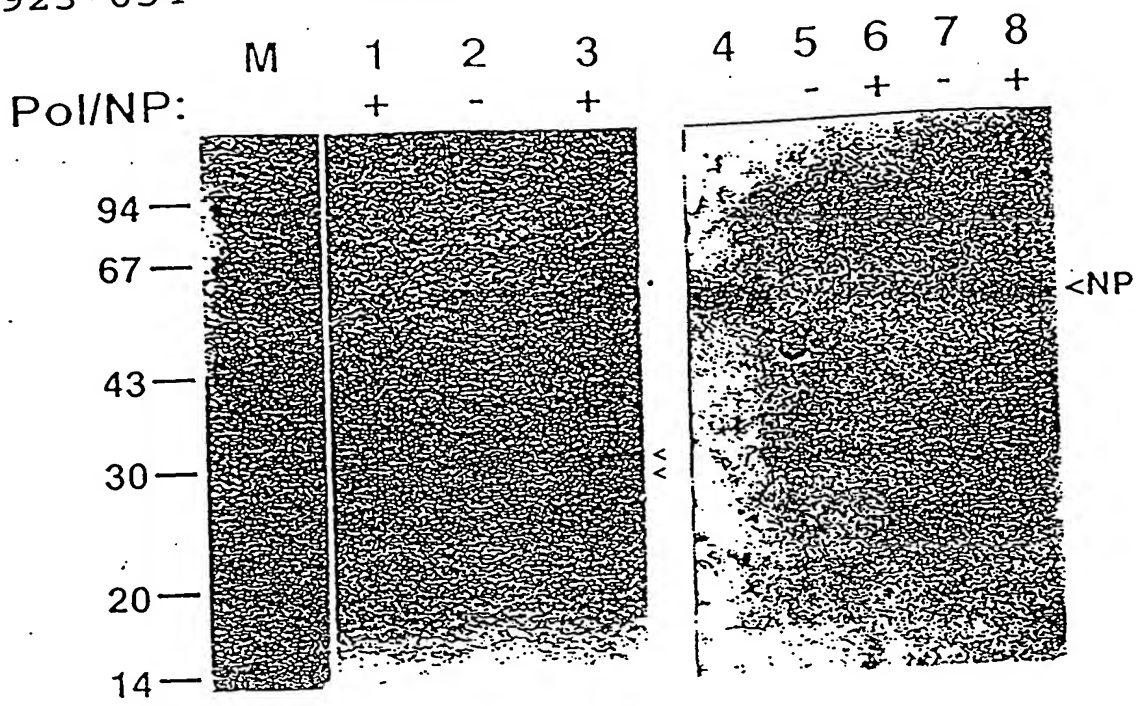
M
1
2
3
4
5
6
7
8
Pol/NP:
+
-
+
-
+
-
+
94
67
43
30
20
14
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FIG. 4

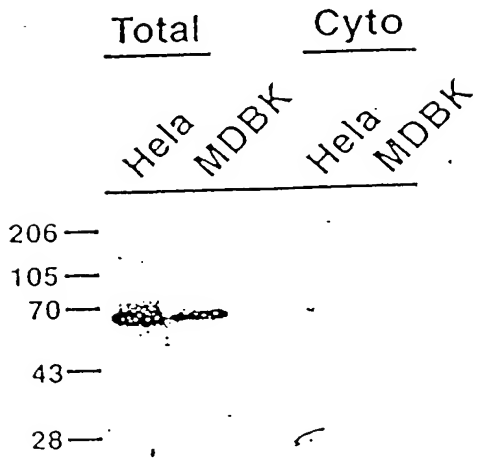

Total
Cyto
Hela
MDBK
Hela
MDBK
206
105
70
43
28

FIG. 5

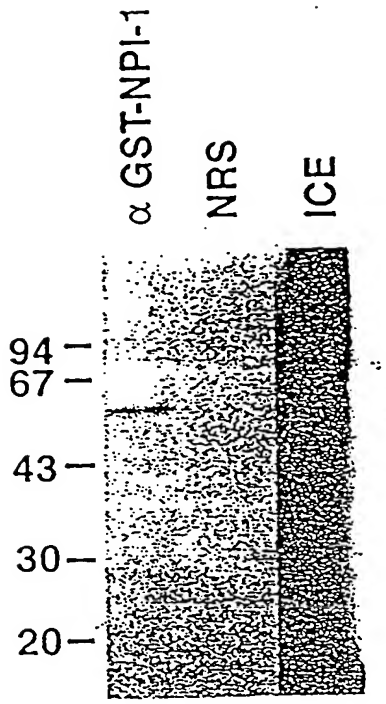


FIG. 6

```
                    20                  40                  60
GGAGGCACCG AAGGGCAGCG CCGAGTCGGA GGGGGCGAAG ATTGACGCCA GTAAGAACGA

                    80                  100                 120
GGAGGATGAA GGCCATTCAA ACTCCTCCCC ACGACACTCT GAAGCAGCGA CGGCACAGCG

                   140                  160
GGAAGAATGG AAAATGTTTA TAGGAGGCCT TAGCTGGGAC ACTACAAAGA
```

FIG. 7

```
                    20                  40                  60
GAGGTCAATG TGGAGCTGAG GAAAGCTAAG AAGGATGACC AGATGCTGAA GAGGAGAAAT
 E  V  N   V  E  L  R   K  A  K   K  D  D   Q  M  L  K   R  R  N>

                    80                 100                 120
GTAAGCTCAT TTCCTGATGA TGCTACTTCT CCGCTGCAGG AAAACCGCAA CAACCAGGGC
 V  S  S   F  P  D  D   A  T  S   P  L  Q   E  N  R  N   N  Q  G>

                   140                 160                 180
ACTGTAAATT GGTCTGTTGA TGACATTGTC AAAGGCATAA ATAGCAGCAA TGTGGAAAAT
 T  V  N   W  S  V  D   D  I  V   K  G  I   N  S  S  N   V  E  N>

                   200                 220                 240
CAGCTCCAAG CTACTCAAGC TGCCAGGAAA CTACTTTCCA GAGAAAAACA GCCCCCCATA
 Q  L  Q   A  T  Q  A   A  R  K   L  L  S   R  E  K  Q   P  P  I>

                   260                 280                 300
GACAACATAA TCCGGGCTGG TTTGATTCCG AAATTTGTGT CCTTCTTGGG CAGAACTGAT
 D  N  I   I  R  A  G   L  I  P   K  F  V   S  F  L  G   R  T  D>

                   320                 340                 360
TGTAGTCCCA TTCAGTTTGA ATCTGCTTGG GCACTCACTA ACATTGCTTC TGGGACATCA
 C  S  P   I  Q  F  E   S  A  W   A  L  T   N  I  A  S   G  T  S>

                   380                 400                 420
GAACAAACCA AGGCTGTGGT AGATGGAGGT GCCATCCCAG CATTCATTTC TCTGTTGGCA
 E  Q  T   K  A  V  V   D  G  G   A  I  P   A  F  I  S   L  L  A>

                   440                 460                 480
TCTCCCCATG CTCACATCAG TGAACAAGCT GTCTGGGCTC TAGGAAACAT TGCAGGTGAT
 S  P  H   A  H  I  S   E  Q  A   V  W  A   L  G  N  I   A  G  D>

                   500                 520                 540
GGCTCAGTGT TCCGAGACTT GGTTATTAAG TACGGTGCAG TTGACCCACT GTTGGCTCTC
 G  S  V   F  R  D  L   V  I  K   Y  G  A   V  D  P  L   L  A  L>

                   560                 580                 600
CTTGCAGTTC CTGATATGTC ATCTTTAGCA TGTGGCTACT TACGTAATCT TACCTGGACA
 L  A  V   P  D  M  S   S  L  A   C  G  Y   L  R  N  L   T  W  T>

                   620                 640                 660
CTTTCTAATC TTTGCCGCAA CAAGAATCCT GCACCCCCGA TAGATGCTGT TGAGCAGATT
 L  S  N   L  C  R  N   K  N  P   A  P  P   I  D  A  V   E  Q  I>

                   680                 700                 720
CTTCCTACCT TAGTTCGGCT CCTGCATCAT GATGATCCAG AAGTGTTAGC AGATACCTGC
 L  P  T   L  V  R  L   L  H  H   D  D  P   E  V  L  A   D  T  C>

                   740                 760                 780
TGGGCTATTT CCTACCTTAC TGATGGTCCA AATGAACGAA TTGGCATGGT GGTGAAAACA
 W  A  I   S  Y  L  T   D  G  P   N  E  R   I  G  M  V   V  K  T>
```

FIG. 8A

```
                    800                 820                 840
GGAGTTGTGC CCCAACTTGT GAAGCTTCTA GGAGCTTCTG AATTGCCAAT TGTGACTCCT
 G  V  V   P  Q  L  V   K  L  L   G  A  S   E  L  P  I   V  T  P>

                    860                 880                 900
GCCCTAAGAG CCATAGGGAA TATTGTCACT GGTACAGATG AACAGACTCA GGTTGTGATT
 A  L  R   A  I  G  N   I  V  T   G  T  D   E  Q  T  Q   V  V  I>

                    920                 940                 960
GATGCAGGAG CACTCGCCGT CTTTCCCAGC CTGCTCACCA ACCCCAAAAC TAACATTCAG
 D  A  G   A  L  A  V   F  P  S   L  L  T   N  P  K  T   N  I  Q>

                    980                1000                1020
AAGGAAGCTA CGTGGACAAT GTCAAACATC ACAGCCGGCC GCCAGGACCA GATACAGCAA
 K  E  A   T  W  T  M   S  N  I   T  A  G   R  Q  D  Q   I  Q  Q>

                   1040                1060                1080
GTTGTGAATC ATGGATTAGT CCCATTCCTT GTCAGTGTTC TCTCTAAGGC AGATTTTAAG
 V  V  N   H  G  L  V   P  F  L   V  S  V   L  S  K  A   D  F  K>

                   1100                1120                1140
ACACAAAAGG AAGCTGTGTG GGCCGTGACC AACTATACCA GTGGTGGAAC AGTTGAACAG
 T  Q  K   E  A  V  W   A  V  T   N  Y  T   S  G  G  T   V  E  Q>

                   1160                1180                1200
ATTGTGTACC TTGTTCACTG TGGCATAATA GAACCGTTGA TGAACCTCTT AACTGCAAAA
 I  V  Y   L  V  H  C   G  I  I   E  P  L   M  N  L  L   T  A  K>

                   1220                1240                1260
GATACCAAGA TTATTCTGGT TATCCTGGAT GCCATTTCAA ATATCTTTCA GGCTGCTGAG
 D  T  K   I  I  L  V   I  L  D   A  I  S   N  I  F  Q   A  A  E>

                   1280                1300                1320
AAACTAGGTG AAACTAGCTG CCCGTCTTCA CAGATTCAAG AACAAGGGAA AAGACAGTAC
 K  L  G   E  T  S  C   P  S  S   Q  I  Q   E  Q  G  K   R  Q  Y>

                   1340                1360                1380
AGAAATGAGG CGTCCGAGGC GTCGCAGAAT AGAGAAACTT AGTATAATGA TTGAAGAATG
 R  N  E   A  S  E  A   S  Q  N   R  E  T>

                   1400                1420                1440
TGGAGGCTTA GACAAAATTG AAGCTCTACA AAACCATGAA AATGAGTCTG TGTATAAGGC

                   1460                1480                1500
TTCGTTAAGC TTAATTGAGA AGTATTTCTC TGTAGAGGAA GAGGAAGATC AAAACGTTGT

                   1520                1540                1560
ACCAGAAACT ACCTCTGAAG GCTACACTTT CCAAGTTCAG GATGGGGCTC CTGGGACCTT

                   1580                1600                1620
TAACTTTTAG ATCATGTAGC TGAGACATAA ATTTGTTGTG TACTACGTTT GGTATTTTGT

                   1640                1660                1680
CTTATTGTTT CTCTACTAAG AACTCTTTCT TAAATGTGGT TTGTTACTGT AGCACTTTTT
```

FIG. 8B

```
                  1700                        1720                        1740
ACACTGAAAC TATACTTGAA CAGTTCCAAC TGTACATACA TACTGTATGA AGCTTGTCCT

                  1760                        1780                        1800
CTGACTAGGT TTCTAATTTC TATGTGGAAT TTCCTATCTT GCAGCATCCT GTAAATAAAC

                  1820
ATTCAAGTCC ACCCTTTTCT TGACTTC
```

FIG. 8C

```
                    20                  40                  60
GAACGACCAA GAGGGTGTTC GACTGCTAGA GCCGAGCAGA AGCGTGCCTA AATCAAAGGA

                    80                  100                 120
ACTTGTTTCT TCAAGCTCTT CTGGCAGTGA TTCTGACAGT GAGGTTGACA AAAAGTTAAG

                    140                 160                 180
CAGGAAAAAG CAAGTTGCTC CAGAAAAACC TGTAAAGAAA CAAAAGACAG GTGAGACTTC

                    200                 220                 240
GAGAGCCCTG TCATCTTCTA AACAGAGCAG CAGCAGCAGA GATGATAACA TGTTTCAGAT

TGGGAAAATG AGGTCAGTT
```

FIG. 9

```
      20                  40                  60
TGTCGACTGT GGCTTTGAGC ATCCGTCAGA AGTCCAGCAT GAGTGCATCC CTCAGGCCAT

                    80                  100                 120
TCTGGGAATG GATGTCCTGT GCCAGGCCAA GTCGGGCATG GGAAAGACAG CAGTGTTTGT

                   140                 160                 180
CTTGGCCACA CTGCAACAGC TGGAGCCAGT TACTGGGCAG GTGTCTGTAC TGGTGATGTG

                   200                 220
TCACACTCGG GAGTTGGCTT TTCAGATCAG CAAGGAATAT G
```

FIG. 10

```
                    20                  40                  60
ATTTGTAAAC CCCGGAGCGA GGTTCTGCTT ACCCGAGGCC GCTGCTGTGC GGAGACCCCC

                    80                  100                 120
GGGTGAAGCC ACCGTCATCA TGTCTGACCA GGAGGCAAAA CCTTCAACTG AGGACTTGGG

                   140                 160                 180
GGATAAGAAG GAAGGTGAAT ATATTAAACT CAAAGTCATT GGACAGGATA GCAGTGAGAT

                   200                 220                 240
TCACTTCAAA GTGAAAATGA CAACACATCT CAAGAAACTC AAAGAATCAT ACTGTCAAAG

                   260                 280                 300
ACAGGGTGTT CCAATGAATT CACTCAGGTT TCTCTTTGAG GGTCAGAGAA TTGCTGATAA

                   320                 340                 360
TCATACTCCA AAAGAACTGG GAATGGAGGA AGAAGTTGTG ATTGAAGTTT ATCAGGAACA

AACGGGGGGT CA
```

FIG. 11

```
                                                                    -103  TCTGACCCTCGTCCCGCCCCCGC  -80

-81  CATTCGCCGCCTCCTCCTGTCCCGCAGTCGGCGTCCAGCGGCTCTGCTTGTTCGTGTGTGTGTCGTTGCAGGCCTTATTC  -1

1    ATGGGCTCACCGCTGAGGTTCGACGGGCGGGTGGTACTGGTCACCGGCGCGGGGGCAGGATTGGGCCGAGCCTATGCCCT   80
       M  G  S  P  L  R  F  D  G  R  V  V  L  V  T  G  A  G  A  G  L  G  R  A  Y  A  L   27

81   GGCTTTTGCAGAAAGAGGAGCGTTAGTTGTTGTGAATGATTTGGGAGGGGACTTCAAAGGAGTTGGTAAAGGCTCCTTAG  160
       A  F  A  E  R  G  A  L  V  V  V  N  D  L  G  G  D  F  K  G  V  G  K  G  S  L    53

161  CTGATAAGGTTGTTGAAGAAATAAGAAGGAGAGGTGGAAAAGCAGTGGCCAACTATGATTCAGTGGAAGAAGGAGAGAAG  240
       A  D  K  V  V  E  E  I  R  R  R  G  G  K  A  V  A  N  Y  D  S  V  E  E  G  E  K   80

241  GTTGTGAAGACAGCCCTGGATGCTTTTGGAAGAATAGATGTTGTGGTCAACAATGCTGGAATTCTGAGGGATCATTCCTT  320
       V  V  K  T  A  L  D  A  F  G  R  I  D  V  V  V  N  N  A  G  I  L  R  D  H  S  F  107

321  TGCTAGGATAAGTGATGAAGACTGGGATATAATCCACAGAGTTCATTTGCGGGGTTCATTCCAAGTGACACGGGCAGCAT  400
       A  R  I  S  D  E  D  W  D  I  I  H  R  V  H  L  R  G  S  F  Q  V  T  R  A  A   133

401  GGGAACACATGAAGAAACAGAAGTATGGAAGGATTATTATGACTTCATCAGCTTCAGGAATATATGGCAACTTTGGCCAG  480
       W  E  H  M  K  K  Q  K  Y  G  R  I  I  M  T  S  S  A  S  G  I  Y  G  N  F  G  Q  160

481  GCCAATTATAGTGCTGCAAAGTTGGGTCTTCTGGGCCTTGCAAATTCTCTTGCAATTGAAGGCAGGAAAAGCAACATTCA  560
       A  N  Y  S  A  A  K  L  G  L  L  G  L  A  N  S  L  A  I  E  G  R  K  S  N  I  H  187

561  TTGTAACACCATTGCTCCTAATGCGGGATCACGGATGACTCAGACAGTTATGCCTGAAGATCTTGTGGAAGCCTTGAAGC  640
       C  N  T  I  A  P  N  A  G  S  R  M  T  Q  T  V  M  P  E  D  L  V  E  A  L  K   213

641  CAGAGTATGTGGCACCTCTTGTCCTTTGGCTTTGTCACGAGAGTTGTGAGGAGAATGGTGGCTTGTTTGAGGTTGGTGCA  720
       P  E  Y  V  A  P  L  V  L  W  L  C  H  E  S  C  E  E  N  G  G  L  F  E  V  G  A  240

721  GGATGGATTGGAAAATTACGCTGGGAGCGGACTCTTGGAGCTATTGTAAGACAAAAGAATCACCCAATGACTCCTGAGGC  800
       G  W  I  G  K  L  R  W  E  R  T  L  G  A  I  V  R  Q  K  N  H  P  M  T  P  E  A  267

801  AGTCAAGGCTAACTGGAAGAAGATCTGTGACTTTGAGAATGCCAGCAAGCCTCAGAGTATCCAAGAATCAACTGGCAGTA  880
       V  K  A  N  W  K  K  I  C  D  F  E  N  A  S  K  P  Q  S  I  Q  E  S  T  G  S   293

881  TAATTGAAGTTCTGAGTAAAATAGATTCAGAAGGAGGAGTTTCAGCAAATCATACTAGTCGTGCAACGTCTACAGCAACA  960
       I  I  E  V  L  S  K  I  D  S  E  G  G  V  S  A  N  H  T  S  R  A  T  S  T  A  T  320

961  TCAGGATTTGCTGGAGCTATTGGCCAGAAACTCCCTCCATTTTCTTATGCTTATACGGAACTGGAAGCTATTATGTATGC 1040
       S  G  F  A  G  A  I  G  Q  K  L  P  P  F  S  Y  A  Y  T  E  L  E  A  I  M  Y  A  347

1041 CCTTGGAGTGGGAGCGTCAATCAAGGATCCAAAAGATTTGAAATTTATTTATGAAGGAAGTTCTGATTTCTCCTGTTTGC 1120
       L  G  V  G  A  S  I  K  D  P  K  D  L  K  F  I  Y  E  G  S  S  D  F  S  C  L   373

1121 CCACCTTCGGAGTTATCATAGGTCAGAAATCTATGATGGGTGGAGGATTAGCAGAAATTCCTGGACTTTCAATCAACTTT 1200
       P  T  F  G  V  I  I  G  Q  K  S  M  M  G  G  G  L  A  E  I  P  G  L  S  I  N  F  400

1201 GCAAAGGTTCTTCATGGAGAGCAGTACTTAGAGTTATATAAACCACTTCCCAGAGCAGGAAAATTAAAATGTGAAGCAGT 1280
       A  K  V  L  H  G  E  Q  Y  L  E  L  Y  K  P  L  P  R  A  G  K  L  K  C  E  A  V  427

1281 TGTTGCTGATGTCCTAGATAAAGGATCCGGTGTAGTGATTATTATGGATGTCTATTCTTATTCTGAGAAGGAACTTATAT 1360
       V  A  D  V  L  D  K  G  S  G  V  V  I  I  M  D  V  Y  S  Y  S  E  K  E  L  I   453

1361 GCCACAATCAGTTCTCTCTCTTTCTTGTTGGCTCTGGAGGCTTTGGTGGAAAACGGACATCAGACAAAGTCAAGGTAGCT 1440
       C  H  N  Q  F  S  L  F  L  V  G  S  G  G  F  G  G  K  R  T  S  D  K  V  K  V  A  480
```

FIG. 12A

```
1441 GTAGCCATACCTAATAGACCTCCTGATGCTGTACTTACAGATACCACCTCTCTTAATCAGGCTGCTTTGTACCGCCTCAG 1520
      V  A  I  P  N  R  P  P  D  A  V  L  T  D  T  T  S  L  N  Q  A  A  L  Y  R  L  S  507

1521 TGGAGACCGGAATCCCTTACACATTGATCCTAACTTTGCTAGTCTAGCAGGTTTTGACAAGCCCATATTACATGGATTAT 1600
       G  D  R  N  P  L  H  I  D  P  N  F  A  S  L  A  G  F  D  K  P  I  L  H  G  L   533

1601 GTACATTTGGATTTTCTGCCAGGCGTGTGTTACAGCAGTTTGCAGATAATGATGTGTCAAGATTCAAGGCAGTTAAGGCT 1680
      C  T  F  G  F  S  A  R  R  V  L  Q  Q  F  A  D  N  D  V  S  R  F  K  A  V  K  A  560

1681 CGTTTTGCAAAACCAGTATATCCAGGACAAACTCTACAAACTGAGATGTGGAAGGAAGGAAACAGAATTCATTTTCAAAC 1760
      R  F  A  K  P  V  Y  P  G  Q  T  L  Q  T  E  M  W  K  E  G  N  R  I  H  F  Q  T  587

1761 CAAGGTCCAAGAAACTGGAGACATTGTCATTTCAAATGCATATGTGGATCTTGCACCAACATCTGGTACTTCAGCTAAGA 1840
       K  V  Q  E  T  G  D  I  V  I  S  N  A  Y  V  D  L  A  P  T  S  G  T  S  A  K   613

1841 CACCCTCTGAGGGCGGGAAGCTTCAGAGTACCTTTGTATTTGAGGAAATAGGACGCCGCCTAAAGGATATTGGGCCTGAG 1920
      T  P  S  E  G  G  K  L  Q  S  T  F  V  F  E  E  I  G  R  R  L  K  D  I  G  P  E  640

1941 GTGGTGAAGAAAGTAAATGCTGTATTTGAGTGGCATATAACCAAAGGCGGAAATATTGGGGCTAAGTGGACTATTGACCT 2000
      V  V  K  K  V  N  A  V  F  E  W  H  I  T  K  G  G  N  I  G  A  K  W  T  I  D  L  667

2001 GAAAAGTGGTTCTGGAAAAGTGTACCAAGGCCCTGCAAAAGGTGCTGCTGATACAACAATCATACTTTCAGATGAAGATT 2080
       K  S  G  S  G  K  V  Y  Q  G  P  A  K  G  A  A  D  T  T  I  I  L  S  D  E  D   693

2081 TCATGGAGGTGGTCCTGGGCAAGCTTGACCCTCAGAAGGCATTCTTTAGTGGCAGGCTGAAGGCCAGAGGGAACATCATG 2160
      F  M  E  V  V  L  G  K  L  D  P  Q  K  A  F  F  S  G  R  L  K  A  R  G  N  I  M  720

2161 CTGAGCCAGAAACTTCAGATGATTCTTAAAGACTACGCCAAGCTCTGAAGGGCACACTACACTATTAATAAAAATGGAAT 2240
       L  S  Q  K  L  Q  M  I  L  K  D  Y  A  K  L                                    735

2241 CATTAAATACTCTCTTCACCCAAATATGCTTGATTATTCTGCAAAAGTGATTAGAACTAAGATGCAGGGGAAATTGCTTA 2320

2340 ACATTTTCAGATATCAGATAACTGCAGATTTTCATTTTCTACTAATTTTTCATGTATCATTATTTTTACAAGGAACTATA 2400

2401 TATAAGCTAGCACATAATTATCCTTCTGTTCTTAGATCTGTATCTTCATAATAAAAAAATTTTGCCCAAGTCCTGTTTCC 2480

2480 TTAGAATTTGTGATAGCATTGATAAGTTGAAAGGAAAATTAAATCAATAAAGGCCTTTGATACCTTTAAAAAAAAAAAAA 2560

     AAAAAAAAAAAA
```

FIG. 12B

FIG. 13

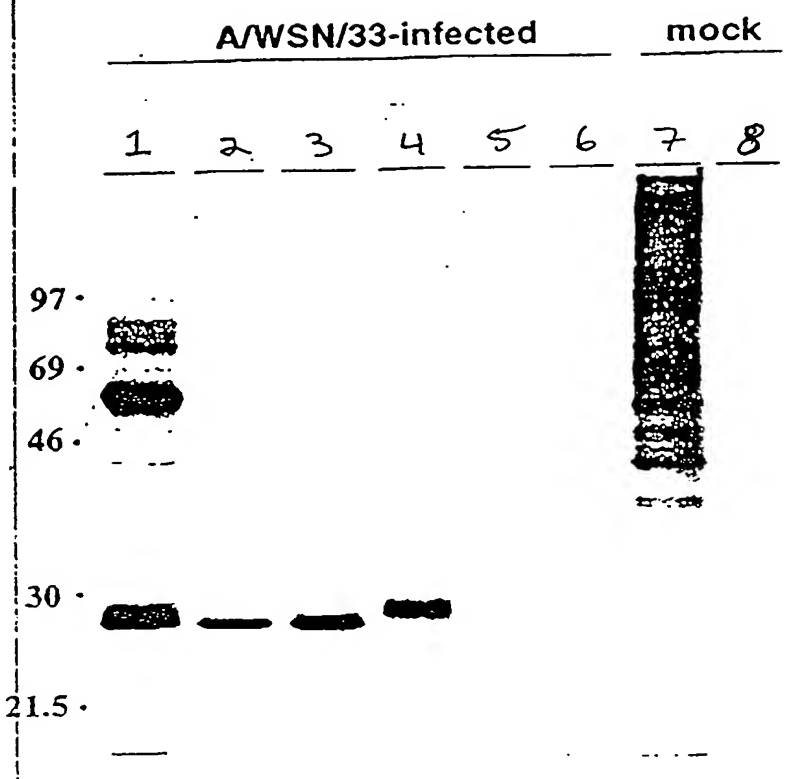


FIG. 14

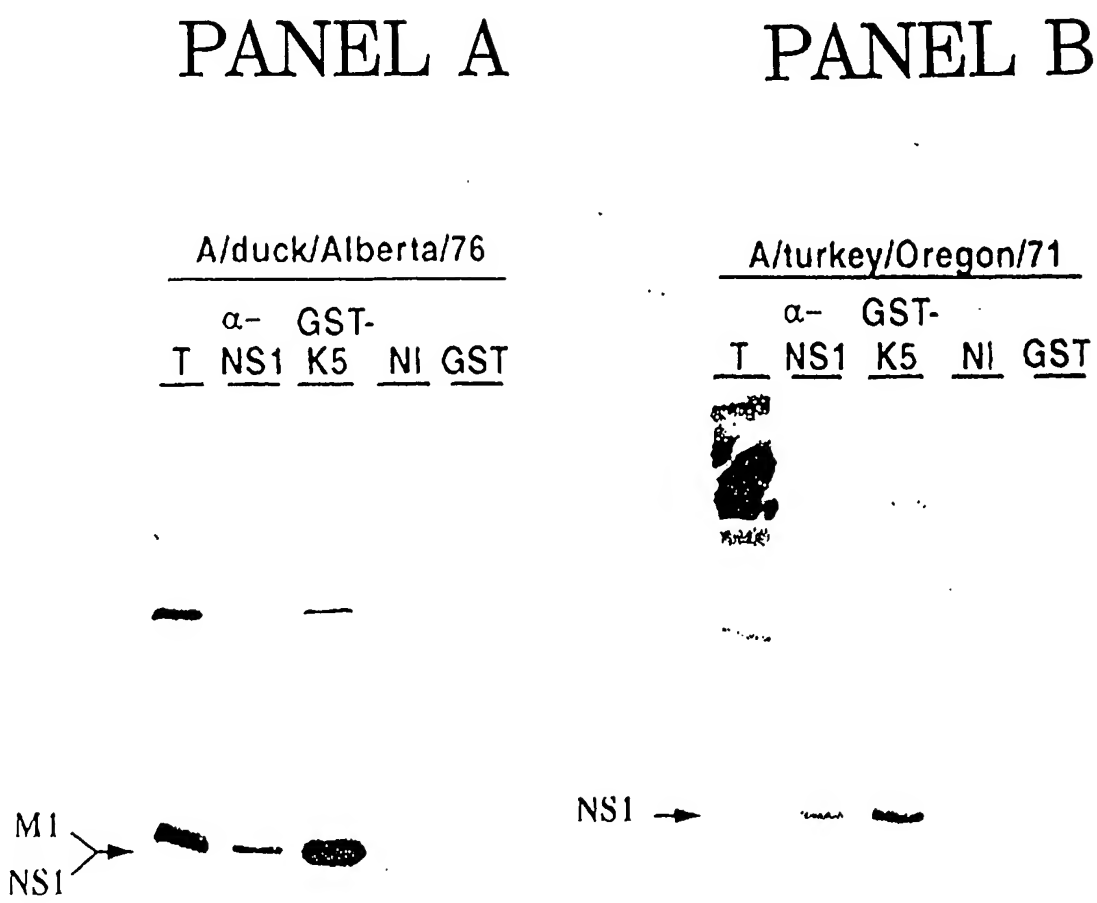
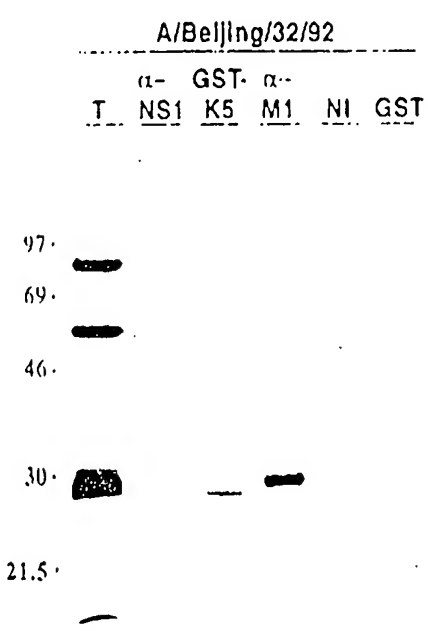
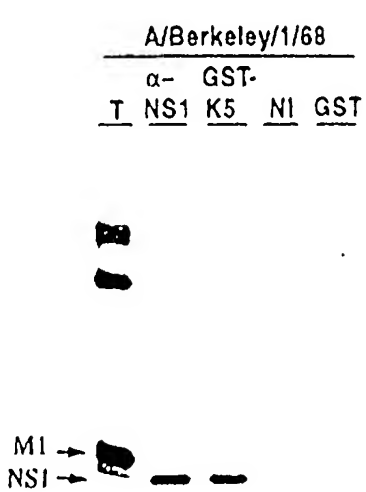

PANEL A
PANEL B
A/duck/Alberta/76
A/turkey/Oregon/71
α- GST-
T NS1 K5 NI GST
T NS1 K5 NI GST
M1
NS1
NS1

FIG. 15A

PANEL C



PANEL D



PANEL E

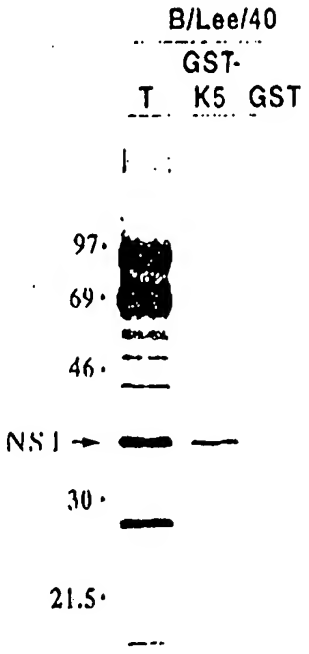


FIG. 15B